Kcnh7 Cas9-CKO Strategy matech Co. Ltd Cenphamare, Rondhamater Co.

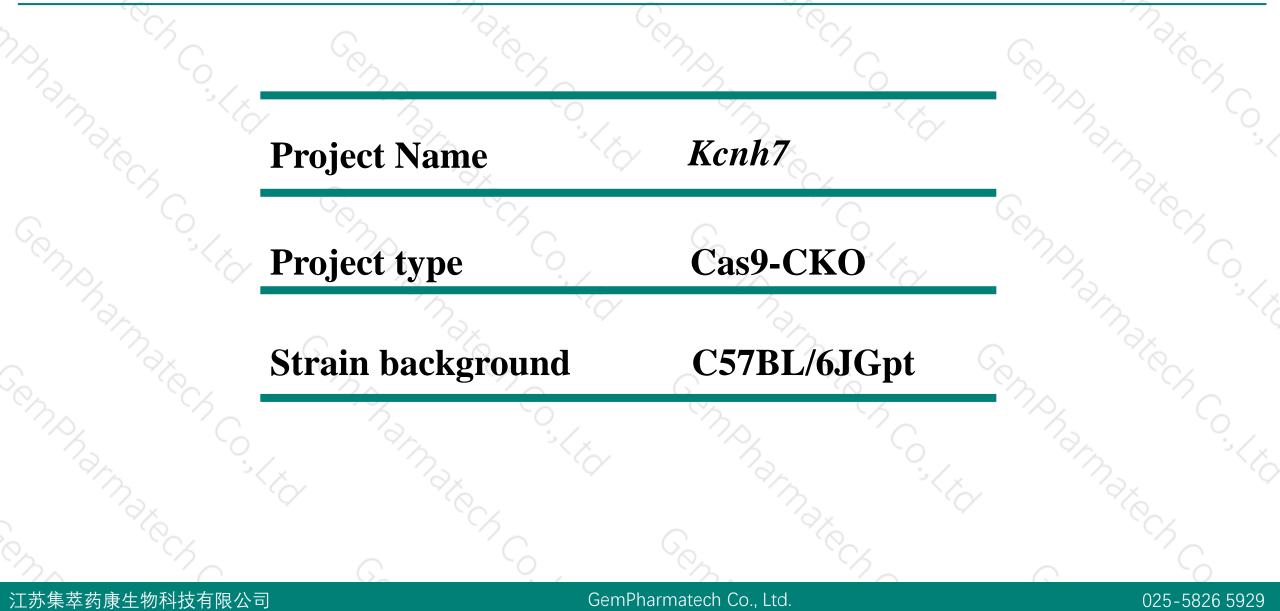
Designer: Emphamaten C. 1 t

Qiong Zhou

Genpharman

Project Overview

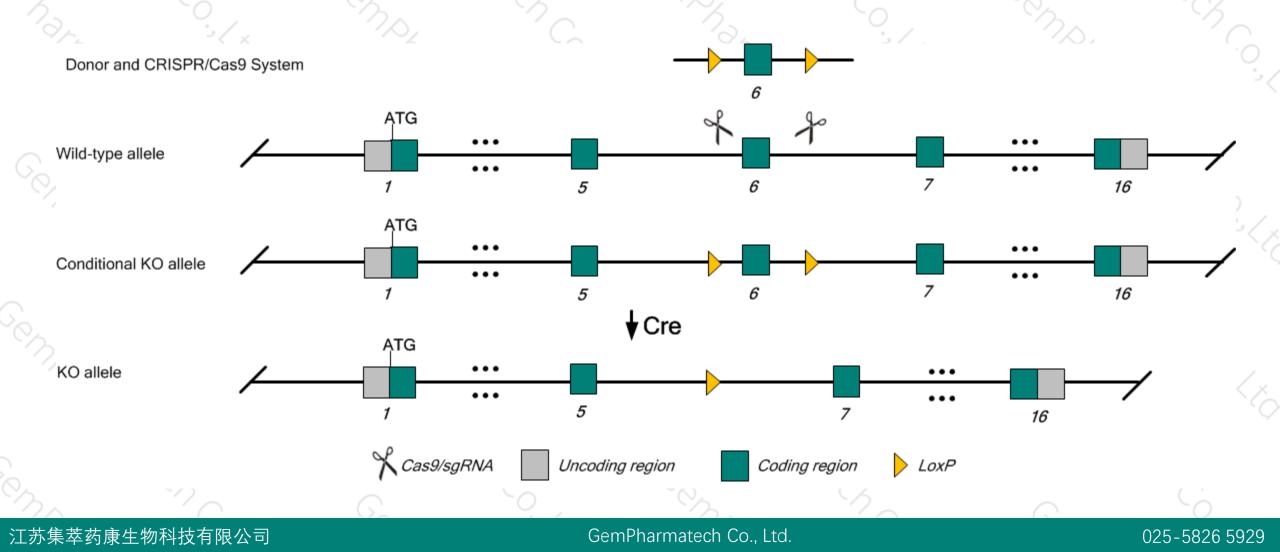




Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Kcnh7 gene. The schematic diagram is as follows:





- The Kcnh7 gene has 4 transcripts, According to the structure of Kcnh7 gene, exon6 of Kcnh7-201 transcript is recommended as the knockout region. The region contains the 215bp coding seqence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Kcnh7* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed.Cas9, sgRNA and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- The flox mice was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues or cell types.

- The *Kcnh7* gene is located on the Chr2. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This Strategy is designed based on genetic information in existing databases.Due to the complexity of biological processes, all risk of the loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Notice

Gene information (NCBI)



Kcnh7 potassium voltage-gated channel, subfamily H (eag-related), member 7 [*Mus musculus* (house mouse)]

Gene ID: 170738, updated on 31-Jan-2019

Summary

| Official Symbol | Konh7 provided by <u>MGI</u> | | | | | | | |
|--------------------|---|--|--|--|--|--|--|--|
| Official Full Name | potassium voltage-gated channel, subfamily H (eag-related), member 7 provided by <u>MGI</u> | | | | | | | |
| Primary source | MGI:MGI:2159566 | | | | | | | |
| See related | Ensembl:ENSMUSG0000059742 | | | | | | | |
| Gene type | protein coding | | | | | | | |
| RefSeq status | VALIDATED | | | | | | | |
| Organism | Mus musculus | | | | | | | |
| Lineage | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; | | | | | | | |
| | Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus | | | | | | | |
| Also known as | erg3; Kv11.3; 9330137I11Rik | | | | | | | |
| Expression | Biased expression in cortex adult (RPKM 1.9), frontal lobe adult (RPKM 1.4) and 5 other tissues See more | | | | | | | |
| Orthologs | human all | | | | | | | |
| | | | | | | | | |

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Transcript information (Ensembl) 第標語

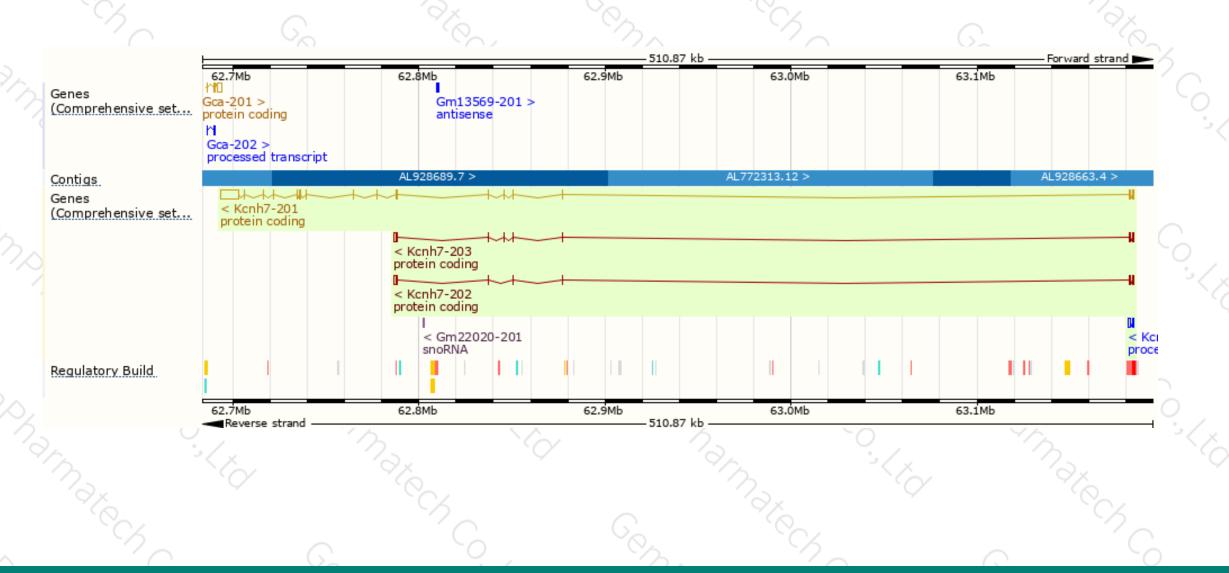
The gene has 4 transcripts, and all transcripts are shown below :

| 🗧 Name 🍦 | Transcript ID 🛛 🍦 | bp 🌲 | Protein 🖕 | Biotype 🍦 | CCDS 🖕 | UniProt 🍦 | RefSeq 🍦 | Flags 🍦 |
|-----------|----------------------|-------|---------------|----------------------|--------------------|-----------------|--------------------------------------|-------------------------------|
| Kcnh7-201 | ENSMUST00000075052.9 | 13321 | <u>1195aa</u> | Protein coding | <u>CCDS38128</u> ៤ | <u>Q9ER47</u> ₫ | <u>NM_133207</u> <u>NP_573470</u> | TSL:1 GENCODE basic APPRIS P1 |
| Kcnh7-203 | ENSMUST00000112454.7 | 3073 | <u>522aa</u> | Protein coding | - | <u>Q8CC38</u> 🗗 | - | TSL:1 GENCODE basic |
| Kcnh7-202 | ENSMUST00000112452.1 | 2849 | <u>515aa</u> | Protein coding | - | <u>Q8C782</u> | - | TSL:1 GENCODE basic |
| Kcnh7-204 | ENSMUST00000131799.1 | 1079 | No protein | Processed transcript | - | - | - | TSL:1 |

The strategy is based on the design of *Kcnh7-201* transcript, The transcription is shown below



Genomic location distribution



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Protein domain



| | | | 19X | | | | | 5 | | | $\langle Q \rangle$ | × |
|------------------|---|-------------------------------------|----------------------------|-------------|-------------------|-------------|---------------|----------------------|-----------------|------|---------------------|-----|
| 2× | ENSMUSP0000074 Transmembrane heli MobiDB lite Low complexity (Seg) Conserved Domains Coiled-coils (Ncoils) hmmpanther | PTHR10217 | | - | - | | | | | _ | - | |
| - C | TICDEAM domain | PTHR10217:SF466 | | | | | | | | | | |
| | TIGRFAM domain | PAS domain | | | | | | | | | | |
| | Superfamily domains | PAS domain superfa | nily | SSF8132 | 4 | | Cyclic nucle | otide-binding-lik | e | | | |
| | SMART domains | | | | | | , | yclic nucleotide- | | | | í C |
| | Prints domain | | | | ium channel, volt | | | ychc nucleotide- | binding domain | | | -0 |
| | | | | | n channel, voltag | _ | | | | | | < |
| $\gamma_{r_{a}}$ | Pfam domain | PAS domain | | | sport domain | e-depender | it, EAG/ELK/E | | de-binding doma | ain | | |
| | | | | | | | | | - | | | |
| | PROSITE profiles | | | | | | c | yclic nucleotide- | binding domain | | | 1 |
| | Gene3D | 3.30.450.20 | Vo | ltage-depen | dent channel don | ain superfa | amily RmIC | like jelly roll fold | 1 | | | 2 |
| | | | | | 1.10. | 287.70 | 1.10.1200.2 | 60 | | | | C |
| | All sequence SNPs/i | Sequence variants (db | SNP and all other sources) | | | | | | | | | |
| | Variant Legend | | 1 111 1 | | 1 11 | | | 11 | | 1 11 | | 5 |
| | variant Legenu | missense variant synonymous variant | | | | | | | | | | |
| 1 | Scale bar | 0 100 | 200 300 | 400 | 500 | 600 | 700 | 800 | 900 | 1000 | 1195 | |
| | | | | | | | | | | | | |
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If you have any questions, you are welcome to inquire. Tel: 025-5864 1534



